

1/13

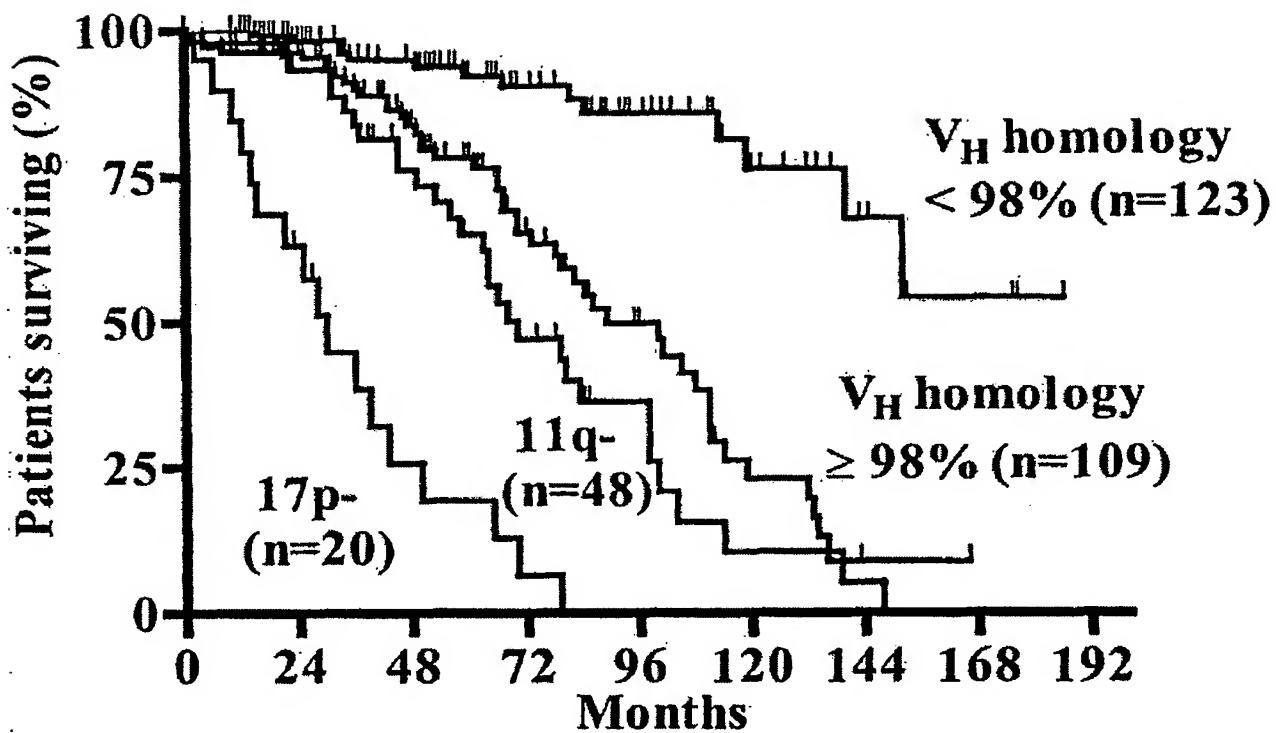


Fig. 1

2/13

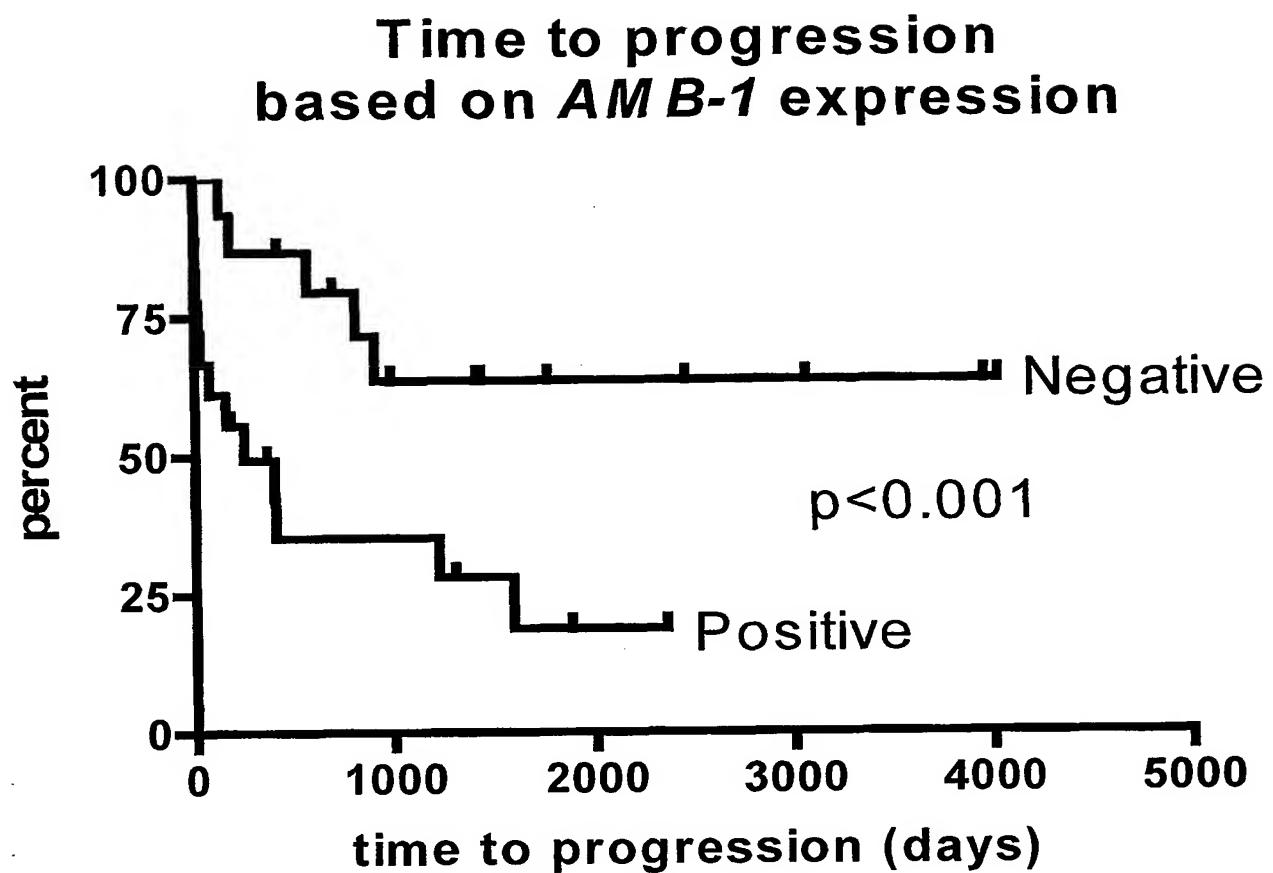


Fig. 2a

3/13

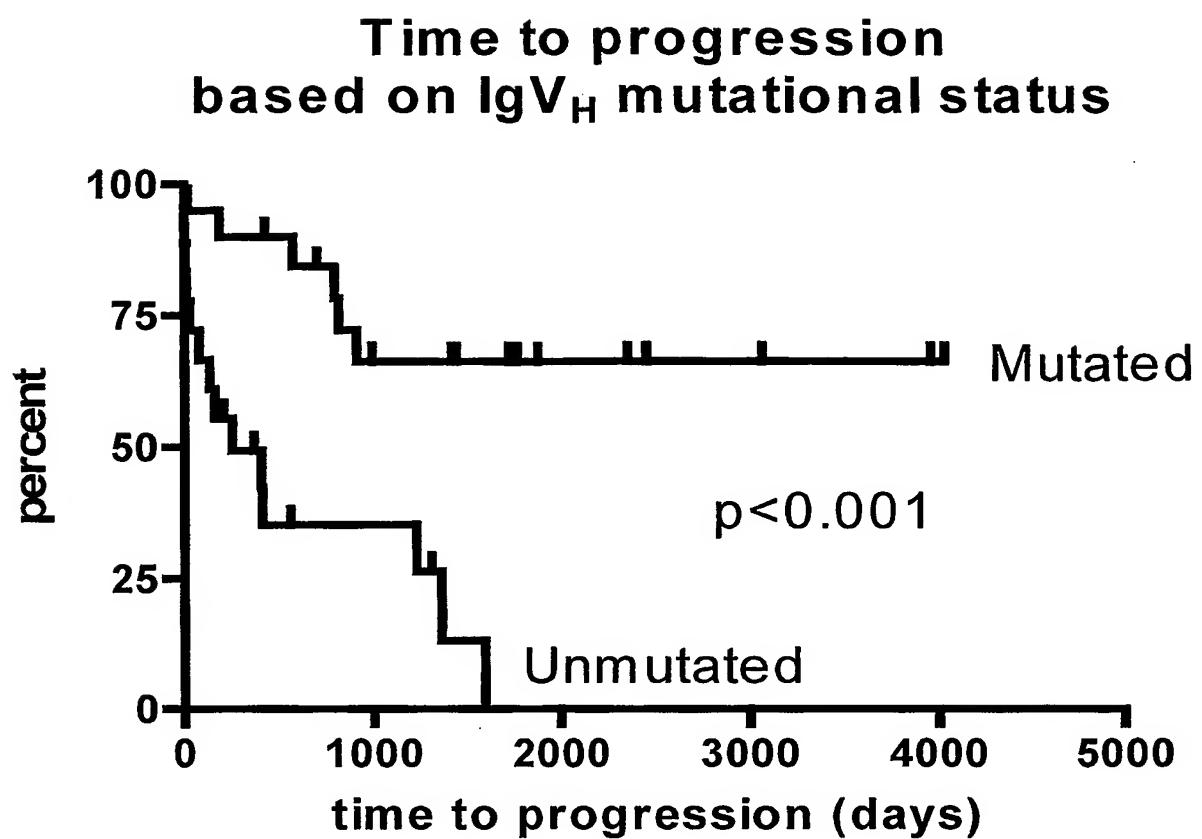


Fig. 2b

4/13

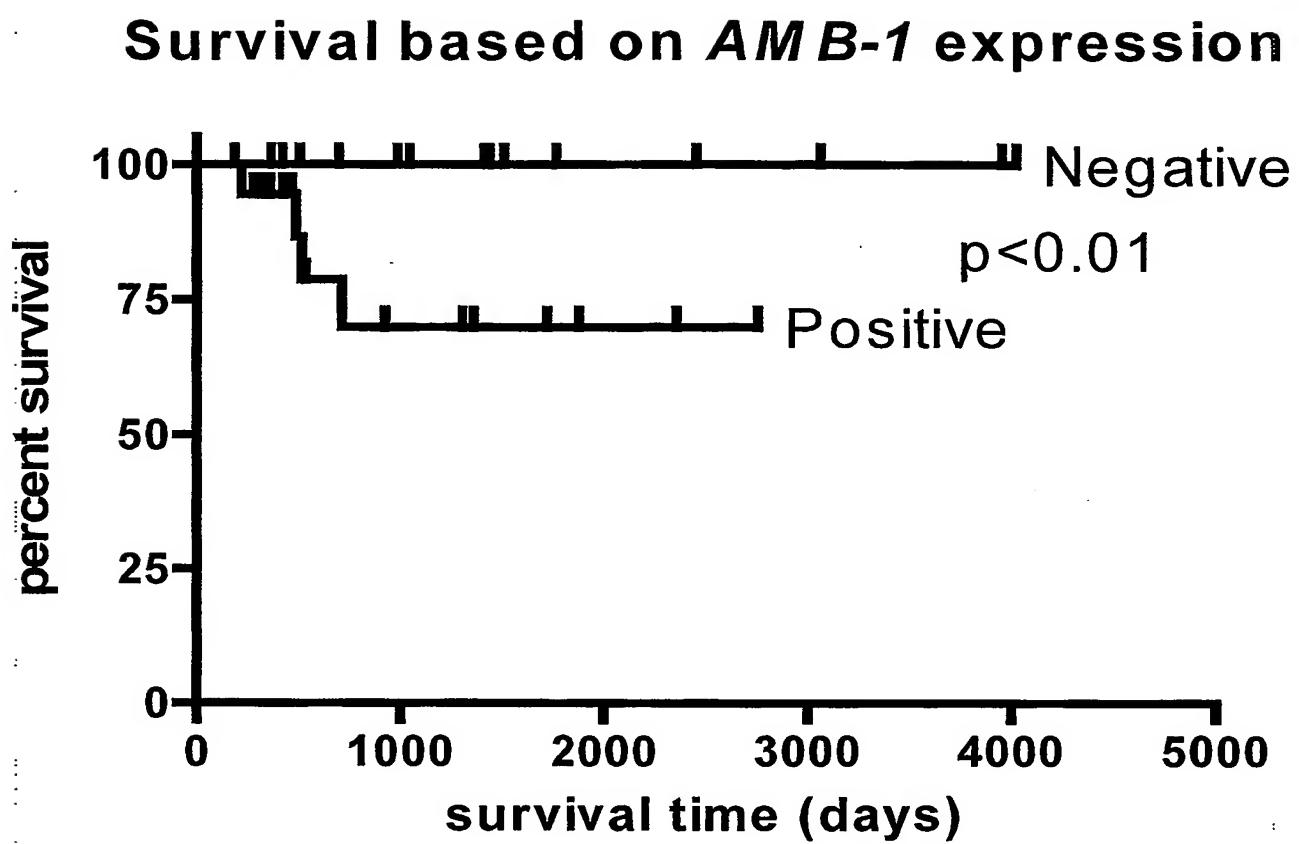


Fig. 2c

5/13

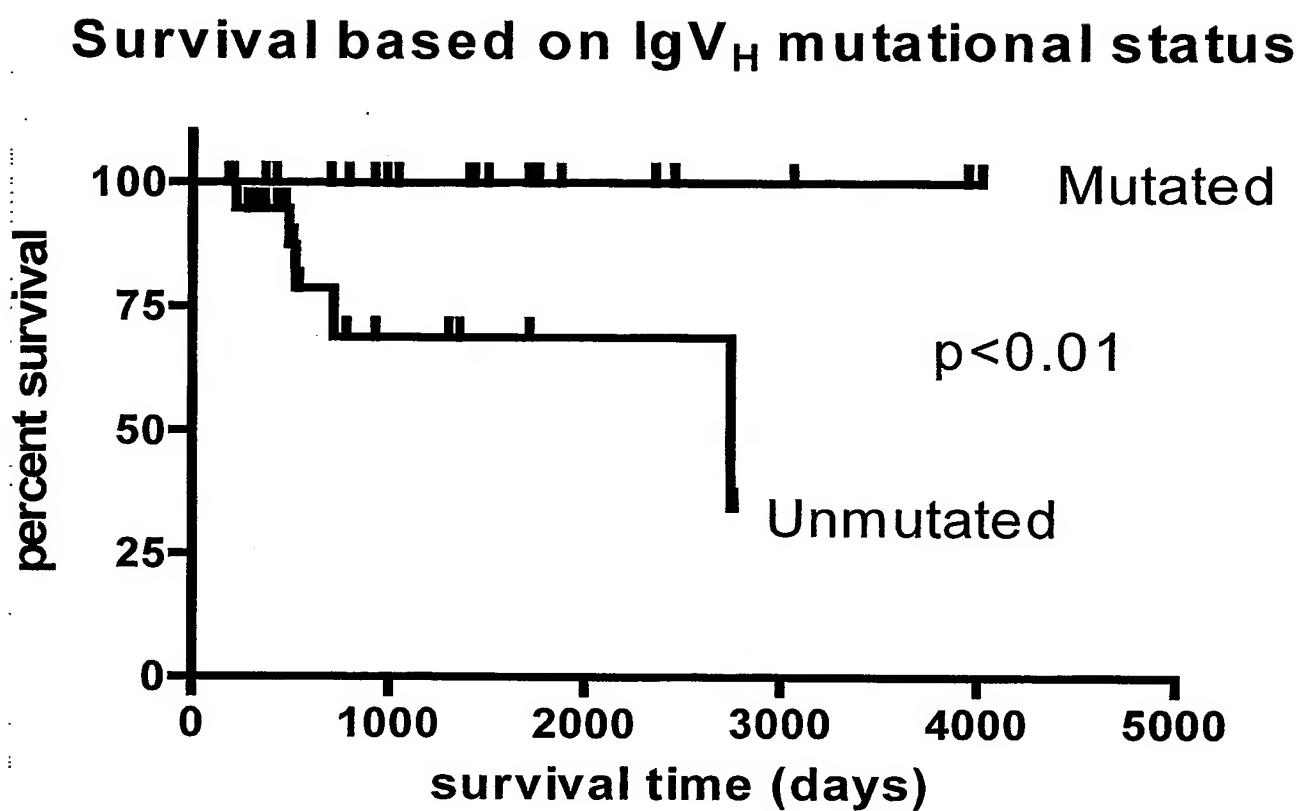


Fig. 2d

6/13

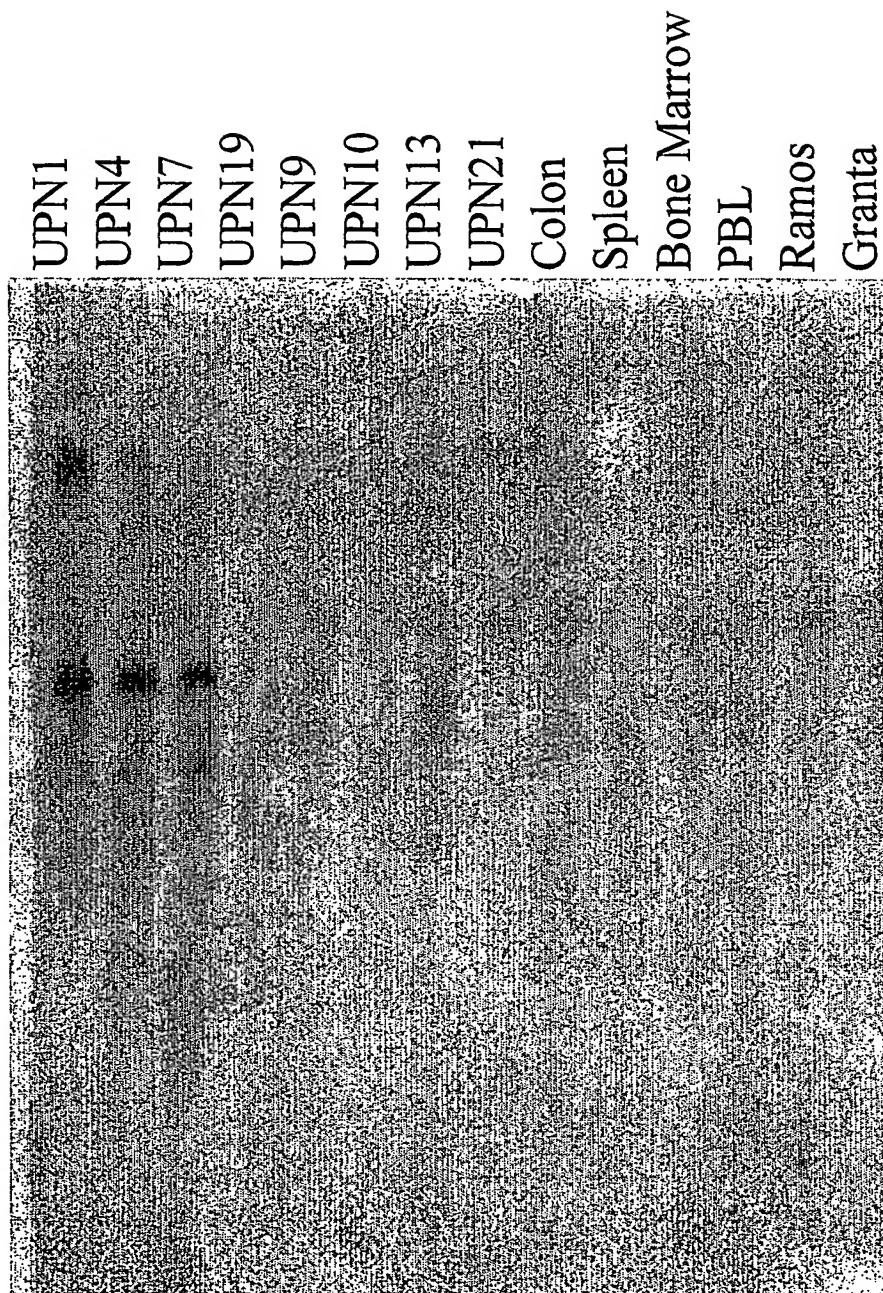


Fig. 3

7/13

AMB1_pe_PSS	CCCCCCCC	HHHEEECCC	CCCCCCCC	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH
AMB1_pe_Seq	MFNKCSFHSS	SSLCAITICFL	NLVIECDLET	NSEINKLIIY	+ - + L - + -	KELCTELTVT	CCCCCCEE						
-----	- - -	--+L--I I -L	-E-	+ -	-	TEQ	HCC						
dliara_Seq	IYRPAADNSA	I T L Q E I I K T L	NSI	HHHHHHHHH	HHH	005	000	000	000	000	000	000	000
dliara_SS	-----	-----	-----	-----	-----	0010040015	0000	0000	0000	0000	0000	0000	0000
CORE	-----	-----	-----	-----	-----	-----	0000	0000	0000	0000	0000	0000	0000
AMB1_pe_PSS	EECCCCCH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH	HHHHHHHH
AMB1_pe_Seq	LFSQNNRIR	F S K L L K I I F	S I F S Y P E	I M C	- - C	K D T R C L G A T A	QQFHRHKQLI	HHHHHHHHHH	HHHHHHHHHH	HHHHHHHHHH	HHHHHHHHHH	HHHHHHHHHH	HHHHHHHHHH
-----	+F+-+	- + - + - -	- + S+-E	- - C	- - C	CCHHHCCCH	0000000000	0000000000	0000000000	0000000000	0000000000	0000000000	0000000000
dliara_Seq	DIFAAASKNT	E K E T F C R A A T	V L R Q F Y S H E	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
dliara_SS	CCCCCCCC	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH
CORE	043000000	0001200920	490030000	490030000	490030000	490030000	490030000	490030000	490030000	490030000	490030000	490030000	490030000
AMB1_pe_PSS	HHHC	CCCCCCC	CCCCCCC	HHHHHH	-----	-----	-----	-----	-----	-----	-----	-----	-----
AMB1_pe_Seq	TFIK	P G I H Y G Q	V S K K H I I Y S	T F L	-----	-----	-----	-----	-----	-----	-----	-----	-----
-----	-F+K	-G+	+ - -	F I L	-----	-----	-----	-----	-----	-----	-----	-----	-----
dliara_Seq	RFLKRLDNL	W G L A G L N S C P	V K E A N Q S T L E	N F L E R L K T I M	-----	-----	-----	-----	-----	-----	-----	-----	-----
dliara_SS	HHHHHHHHH	HHHHHHHHH	CCCCCEEHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH	HHHHHHHHH
CORE	0160080008	0011000000	2000002060	0560080013	0560080013	0560080013	0560080013	0560080013	0560080013	0560080013	0560080013	0560080013	0560080013
AMB1_pe_PSS	EEEEEC	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AMB1_pe_Seq	Q L I R V C W	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
dliara_Seq	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
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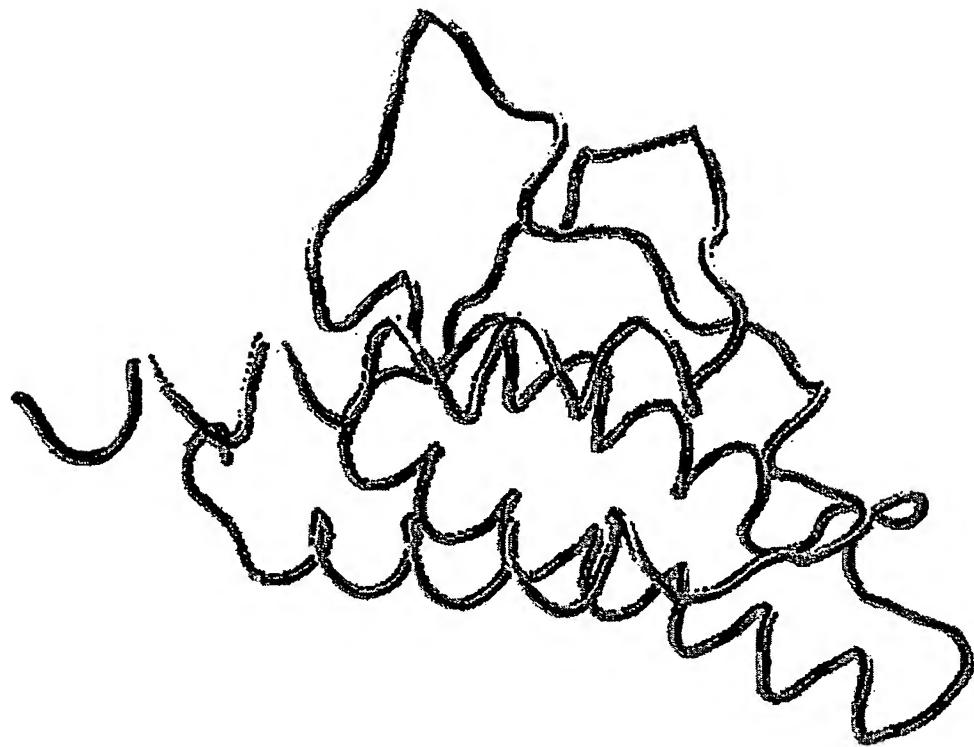
Fig.4

8/13

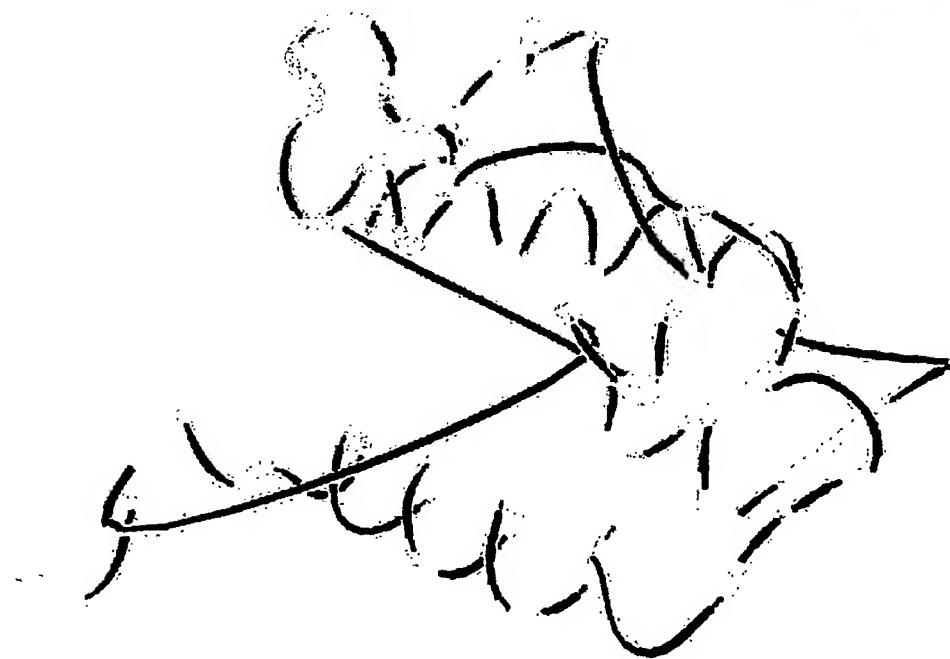
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											Alpha and beta proteins ( $\alpha/\beta$ )	Thioredoxin fold	Thioredoxin-like	Glutathione S- transferase, N- terminal domain	Glutathione S- transferase, N- terminal domain	Interleukin-4 (IL-4)	Short-chain cytokines	PDBTitle: solution structure of 1c5 interleukin-2 1beta generation.	Chain A: PDB Molecule: iceberg (forcefield inhibitor),	Helix-loop-helix DNA-binding domain
d1bp212 23% id.	75		2.88	1	m/a			Alpha and beta proteins ( $\alpha/\beta$ )	Thioredoxin fold	Thioredoxin-like										
d1lara 17% id.	129		3.05	1	m/a			All alpha proteins	4-helical cytokines	4-helical cytokines										
d1ldena 17% id.	89		5.34	1	m/a			Intra SCOP 1.53	PDB header: hydrilase inhibitor.	PDB header: hydrilase inhibitor.										
d1lania 22% id.	80		5.57	1	m/a			b11 alpha proteins	Helix-loop-helix DNA-binding domain	Helix-loop-helix DNA-binding domain										

Fig.5

9/13



Human IL4



AMB1

Fig.6

10/13

AMB1 IIA IL3 IL13 CS-CF  
 AMB1 ---MENKCSFHISSTYRPADNSSECCALICE---IINVIECDE-TNS-EINGLITY-LFSQNNRIRFESKLILKIFI-SIESTYPE---INC---  
 IIA ---HKGCDITLQELIKT---HKCDITLQELIKT---TE-OKI-JACTELJUTDIFASONTIEKETFRATVLSFYSHEKDCR---EQVTFIK---  
 IL3 ---ANGSIMIDE---ILRH---IWRPHPLDEN---IWRPHPLDEN---AGINSCPYKEANQSTLE---NEFLERIAITMPEKYSKSS---  
 IL13 ---NULN-SEONDLMERNURNTNLAFRAVKLENASATES---IKNMLCPL-ATAPTRPHPLIKOG---DANEF---RKOLTYLTKLENDAQOQ  
 CSF ---WALLATTVAUTCGGFASTGMPPTSTARELIEE---IVNI---TONOKAPLGENSERWISI---NUTA-GMCIALESINV---SGCSATEK---TOMLISGCPH-KVSAGQFSSLHYRDKTIEVAF---VCOLLAHAKLKFREGERN  
 IL13 RSFESTQFWERVNIDQERRLLN---SRDFADENETVEVISEM---FDQE-PTCLQTRELXKO---LKGSLIK---GLGSLIK---  
 CSF

Fig. 7

11/13

	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum right	accumbens nucleus	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	HeLa S3	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia K-562	fetal kidney	E.coli rRNA
D	parietal lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	E.coli DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	Poly r(A)
F	temporal lobe	hippo-campus		ventricle right	ilocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human Cot-1 DNA
G	p.g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma SW480	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon, ascending			trachea		lung carcinoma A549	human DNA 500 ng	

Fig. 8

12/13

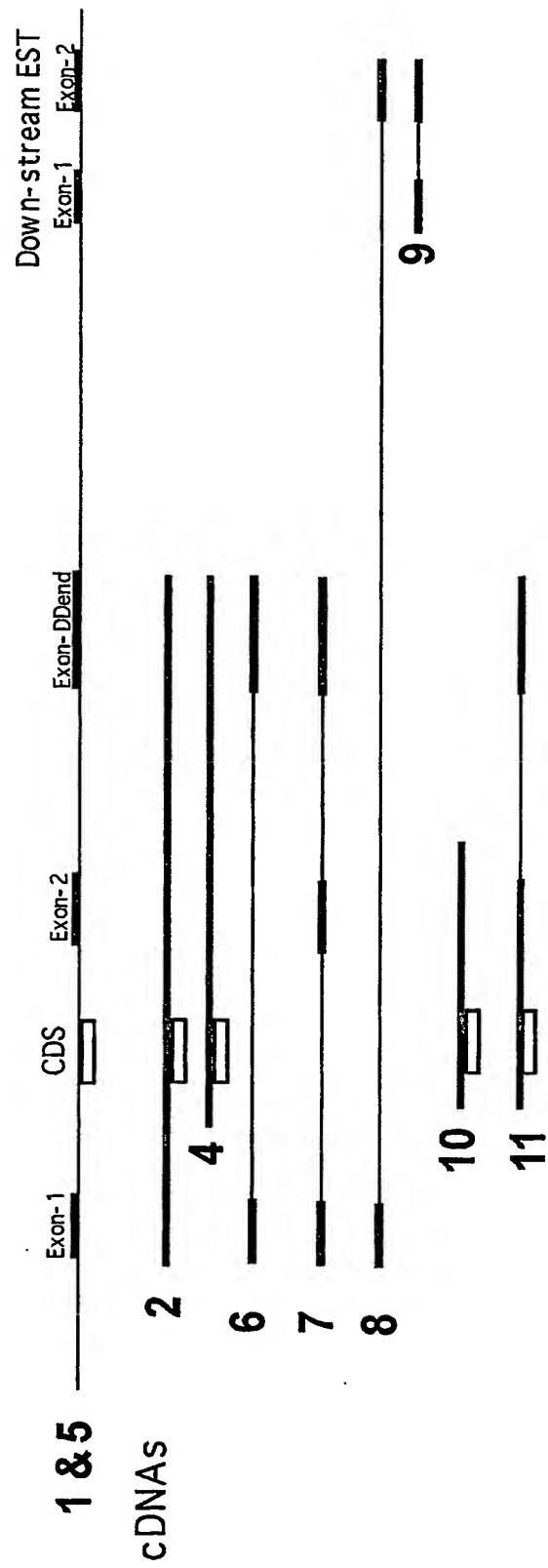


Fig. 9

13/13

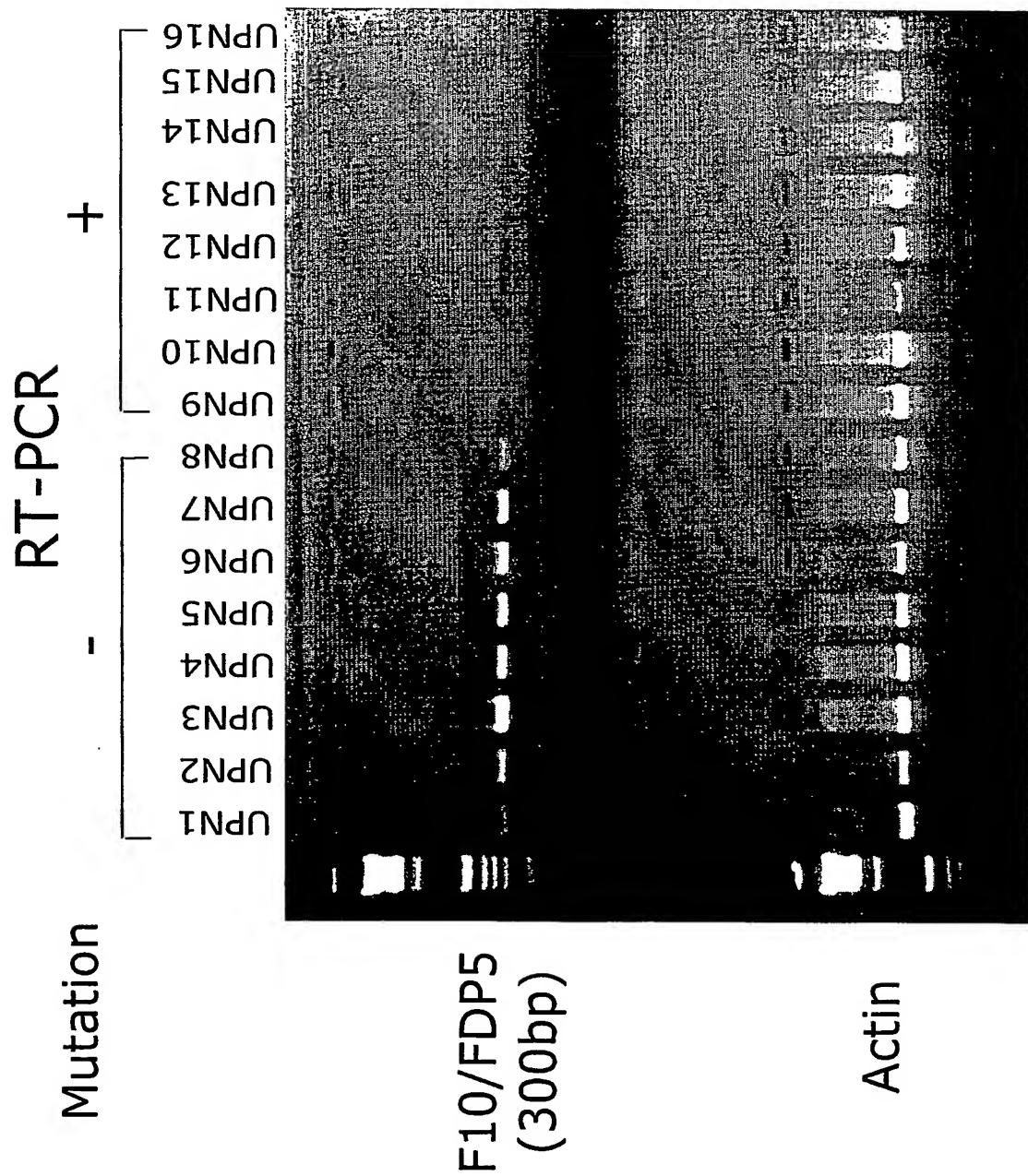


Fig. 10